

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 28, 2003, 18:28:57 ; Search time 13.1515 Seconds  
(without alignments)  
102.373 Million cell updates/sec

Title: US-09-743-225-9

Perfect score: 73

Sequence: 1 KDKATFGTHDGGXA 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_76:\*

1: p1r1.\*

2: p1r2.\*

3: p1r3.\*

4: p1r4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	76.7	345	1 NBHU	apolipoprotein H p
2	46	63.0	345	1 NBMS	apolipoprotein H p
3	42	57.5	574	2 T34208	hypothetical prote
4	42	57.5	1310	2 T40135	oxysterol-binding
5	42	57.5	1674	2 T01265	starch synthase DU
6	41	56.2	297	1 NBRT	apolipoprotein H p
7	41	56.2	345	1 JN0465	apolipoprotein H p
8	40	54.8	345	1 NBBO	apolipoprotein H p
9	40	54.8	363	1 S35733	DNA-directed DNA p
10	40	54.8	1750	2 E86151	hypothetical prote
11	39	53.4	391	2 H84298	2',3'-cyclic-nucle
12	39	53.4	430	2 J8707	hypothetical prote
13	39	53.4	453	2 J87582	armadillo(arm) rep
14	39	53.4	664	2 G84771	probable acyl-CoA
15	39	53.4	1272	2 A10074	probable autotrans
16	39	53.4	1272	2 C96637	hypothetical prote
17	38	52.1	316	2 S19412	hypothetical prote
18	38	52.1	606	2 A72429	oligopeptide ABC t
19	38	52.1	616	2 E83485	probable tonb-depe
20	38	52.1	1772	2 T36105	probable large gly
21	37.5	51.4	966	2 A33626	fibrinogen alpha c
22	37	50.7	160	1 S14574	globin C precursor
23	37	50.7	161	1 S14575	globin D precursor
24	37	50.7	161	1 S14576	globin E precursor
25	37	50.7	163	1 S14572	amidase from nicot
26	37	50.7	216	2 D97119	glucan 1,6-alpha-g
27	37	50.7	537	2 S39970	oligopeptide trans
28	37	50.7	551	2 A13601	hypothetical prote
29	37	50.7	895	2 T34308	hypothetical prote

30	37	50.7	1354	2 AG0538	Rhs-family protein
31	37	50.7	1495	2 S27001	alpha-2-macroglobu
32	37	50.7	2089	2 C85426	ATM-like protein [
33	37	50.7	2632	2 T18718	dynein heavy chain
34	37	50.7	3738	2 T05501	hypothetical prote
35	36	49.3	242	2 S67209	hypothetical prote
36	36	49.3	307	2 G82291	glucokinase regula
37	36	49.3	376	2 AG1550	C-terminal part of
38	36	49.3	417	1 S67566	probable membrane
39	36	49.3	479	2 A25052	fibrinogen beta ch
40	36	49.3	496	2 B41322	N-acetylmuramoyl-L
41	36	49.3	585	2 AC3222	gamma-glutamyltran
42	36	49.3	798	2 S40052	glycogen phosphory
43	35.5	48.6	173	2 AB2205	hypothetical prote
44	35.5	48.6	502	2 A81682	probable thermosta
45	35.5	48.6	502	2 AF1310	probable thermosta

## ALIGNMENTS

### RESULT 1

NBHU

apolipoprotein H precursor [validated] - human

N:Alternate names: activated protein C-binding protein; antidiolipin cofactor; bet

C:Species: Homo sapiens (man)

C>Date: 17-May-1985 #sequence\_revision 30-Jun-1993 #text\_change 08-Dec-2000

C:Accession: S17178; S17668; JQ1379; B43286; A03209; A35786; A46464; I54745; S15499;

R:Steinkasserer, A.; Estaller, C.; Weiss, E.H.; Sim, R.B.; Day, A.J.

Biochem. J. 277, 387-391, 1991

A>Title: Complete nucleotide and deduced amino acid sequence of human beta(2)-glycoprotein

A:Reference number: S17178; MUID:91315408; PMID:1650181

A:Accession: S17178

A:Molecule type: mRNA

A:Residues: 1-345 <STE>

A:Cross-references: EMBL:X58100; NID:G28809; PIDN:CAA41113.1; PID:G28810

R:Kristensen, T.; Schousboe, I.; Boel, E.; Mulvihill, E.M.; Rosendahl Hansen, R.; Bac

FEBS Lett. 289, 183-186, 1991

A>Title: Molecular cloning and mammalian expression of human beta(2)-glycoprotein I c

A:Reference number: S17668; MUID:92008618; PMID:1655523

A:Accession: S17668

A:Molecule type: mRNA

A:Residues: 1-345 <KRI>

A:Cross-references: EMBL:X53595; NID:G28811; PIDN:CAA37664.1; PID:G28812

R:Mehdi, H.; Nunn, M.; Steel, D.M.; Whitehead, A.S.; Perez, M.; Walker, L.; Peeples,

Gene 108, 293-298, 1991

A>Title: Nucleotide sequence and expression of the human gene encoding apolipoprotein

A:Reference number: JQ1379; MUID:92084151; PMID:1748314

A:Accession: JQ1379

A:Molecule type: mRNA

A:Residues: 1-265, 'V', 267-345 <MEH>

A:Cross-references: EMBL:X57847; NID:G28813; PIDN:CAA40977.1; PID:G28814

A:Experimental source: liver

R:Nonaka, M.; Matsuda, Y.; Shirolshi, T.; Moriwaiki, K.; Nonaka, M.; Natsunume-Sakai, S

Genomics 13, 1082-1087, 1992

A>Title: Molecular cloning of mouse beta-2-glycoprotein I and mapping of the gene to

A:Reference number: A33286; MUID:92372000; PMID:1339387

A:Accession: B43286

A>Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-265, 'V', 267-345 <NON>

R:Lozier, J.; Takahashi, N.; Putnam, F.W.

Proc. Natl. Acad. Sci. U.S.A. 81, 3640-3644, 1984

A>Title: Complete amino acid sequence of human plasma beta2-glycoprotein I.

A:Reference number: A03209; MUID:84222015; PMID:6587378

A:Accession: A03209

A:Molecule type: protein

A:Residues: 20-120, 'C', 122-187, 'N', 189-265, 'V', 267-345 <LOZ>

R:McNeill, H.P.; Simpson, R.J.; Chesterman, C.N.; Krillis, S.A.

Proc. Natl. Acad. Sci. U.S.A. 87, 4120-4124, 1990

A>Title: Anti-phospholipid antibodies are directed against a complex antigen that inc

A:Reference number: A35786; MUID:90272666; PMID:2349221

A:Accession: A35786

A:Molecule type: protein  
 A:Residues: 20-22,'X',24-37,'X',39-43 <MCN>  
 R:Natsuura, E.; Igarashi, Y.; Fujimoto, M.; Ichikawa, K.; Suzuki, T.; Sumida, T.; Yasuda, J. Immunol. 148, 3885-3891, 1992  
 A:Title: Heterogeneity of anticardiolipin antibodies defined by the anticardiolipin cofactor  
 A:Reference number: A46464; MUID:92291509; PMID:1602135  
 A:Accession: A46464  
 A:Molecule type: protein  
 A:Residues: 20-44 <MA2>  
 A:Note: sequence extracted from NCBI backbone (NCBIP:105524)  
 R:Natsuura, E.; Igarashi, M.; Igarashi, Y.; Nagae, H.; Ichikawa, K.; Yasuda, T.; Koike, Int. Immunol. 3, 1217-1221, 1991  
 A:Title: Molecular definition of human beta 2-glycoprotein I (beta 2-GPI) by cDNA cloning  
 A:Reference number: I54745; MUID:92135065; PMID:1777418  
 A:Accession: I54745  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-265,'V',267-345 <RES>  
 A:CROSS-references: GB:S80305; NID:9244677; PIDN:AAB21330.1; PID:9244678  
 C:Comment: This plasma glycoprotein is a constituent of chylomicrons, VLDL, and HDL. It is blood coagulation cascade and ADP-mediated platelet aggregation.  
 C:Comment: The physiological role of this protein is uncertain. It may diminish unwanted  
 C:Genetics:  
 A:Gene: GDB:APOH  
 A:CROSS-references: GDB:118887; OMIM:138700  
 A:Map position: 17q23-17qter  
 C:Superfamily: apolipoprotein H; complement factor H repeat homology  
 C:Keywords: chylomicron; duplication; glycoprotein; HDL; heparin binding; lipid binding;  
 F:1-19/Domain: signal sequence #status predicted <SIG>  
 F:20-345/Product: apolipoprotein H #status experimental <MA2>  
 F:23-79/Domain: complement factor H repeat homology <FH1>  
 F:84-137/Domain: complement factor H repeat homology <FH2>  
 F:142-200/Domain: complement factor H repeat homology <FH3>  
 F:205-260/Domain: complement factor H repeat homology <FH4>  
 F:264-325/Domain: complement factor H repeat homology <FH5>  
 F:23-65,51-79,110-137,174-200,205-248,300-307/Disulfide bonds: #status experimental  
 F:84-124,142-188,234-260,264-315,325-345/Disulfide bonds: #status predicted  
 F:162,183,193,253/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 76.7%; Score 56; DB 1; Length 345;  
 Best Local Similarity 90.9%; Pred. No. 0.019;  
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KDKATFGTHDG 11  
 ||||| |||||  
 Db 227 KDKATFGCHDG 237

RESULT 2  
 NBMS  
 apolipoprotein H precursor - mouse  
 N:Alternate names: 50K serum glycoprotein; activated protein C-binding protein; beta-2-glycoprotein I  
 C:Species: Mus musculus (house mouse)  
 C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 28-May-1999  
 C:Accession: A43286; J02243  
 R:Nonaka, M.; Matsuda, Y.; Shirosaki, T.; Moriuchi, K.; Nonaka, M.; Natsuume-Sakai, S. Genomics 13, 1082-1087, 1992  
 A:Title: Molecular cloning of mouse beta-2-glycoprotein I and mapping of the gene to chromosome 13  
 A:Reference number: A43286; MUID:92372000; PMID:1339387  
 A:Accession: A43286  
 A:Molecule type: mRNA  
 A:Residues: 1-252,'A',254-277,'N',279-345 <NON>  
 A:CROSS-references: GB:D10056  
 A:Note: the authors translated the codon ACT for residue 253 as Ala and ATG for residue 254 as Met  
 R:Sellar, G.C.; Steel, D.M.; Zafiroopoulos, A.; Seery, L.T.; Whitehead, A.S. Biochem. Biophys. Res. Commun. 200, 1521-1528, 1994  
 A:Title: Characterization, expression and evolution of mouse beta2-glycoprotein I (apolipoprotein I)  
 A:Reference number: J02243; MUID:94242017; PMID:7514402  
 A:Accession: J02243  
 A:Molecule type: mRNA  
 A:Residues: 1-251,'R',253-345 <SEL>  
 A:CROSS-references: GB:S70439; NID:9546780; PIDN:AAB30789.1; PID:9546781

A:Experimental source: liver  
 C:Genetics:  
 A:Gene: B2gpl  
 A:Map position: 11  
 C:Superfamily: apolipoprotein H; complement factor H repeat homology  
 C:Keywords: chylomicron; duplication; glycoprotein; HDL; heparin binding; lipid binding  
 F:1-19/Domain: signal sequence #status predicted <SIG>  
 F:20-345/Product: apolipoprotein H #status predicted <MA2>  
 F:23-79/Domain: complement factor H repeat homology <FH1>  
 F:84-137/Domain: complement factor H repeat homology <FH2>  
 F:142-200/Domain: complement factor H repeat homology <FH3>  
 F:205-260/Domain: complement factor H repeat homology <FH4>  
 F:264-325/Domain: complement factor H repeat homology <FH5>  
 F:23-65,51-79,84-124,110-137,142-188,174-200,205-248,234-260,264-315,300-307,325-345/Disulfide bonds: #status predicted  
 F:105,117,162,183,193/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 63.0%; Score 46; DB 1; Length 345;  
 Best Local Similarity 80.0%; Pred. No. 1.3;  
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KDKATFGTHD 10  
 ||||| |||||  
 Db 227 KDKATFGCHE 236

RESULT 3  
 T34208  
 hypothetical protein F10E7.9 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999  
 C:Accession: T34208  
 R:Pauley, A.  
 submitted to the EMBL Data Library, November 1995  
 A:Description: The sequence of C. elegans cosmid F10E7.  
 A:Reference number: 221489  
 A:Accession: T34208  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-574 <PAU>  
 A:CROSS-references: EMBL:U41364; PIDN:AA82423.1; CESP:F10E7.9  
 C:Genetics:  
 A:Gene: CESP:F10E7.9  
 A:Introns: 37/2; 110/3; 178/1; 345/3; 468/3; 538/3

Query Match 57.5%; Score 42; DB 2; Length 574;  
 Best Local Similarity 72.7%; Pred. No. 11;  
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 KDKATFGTHDG 11  
 ||||| |||||  
 Db 42 KDKVLFGTWDG 52

RESULT 4  
 T40135  
 oxysterol-binding protein homolog C3F12.05c - fission yeast (Schizosaccharomyces pombe)  
 C:Species: Schizosaccharomyces pombe  
 C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Dec-2002  
 C:Accession: T40135  
 R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.  
 submitted to the EMBL Data Library, June 1997  
 A:Reference number: Z21907  
 A:Accession: T40135  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-1310 <WO>  
 A:CROSS-references: EMBL:997211; PIDN:CAB10154.2; GSPDB:GN00067; SPDB:SPBC2F12.05c  
 A:Experimental source: strain 972h; cosmid c3F12  
 C:Genetics:  
 A:Gene: SPDB:SPBC2F12.05c  
 A:Map position: 2  
 A:Introns: 20/1; 34/1; 91/3  
 C:Superfamily: oxysterol-binding protein homolog OSH1/SWH1; ankyrin repeat homology;

Query Match 57.5%; Score 42; DB 2; Length 1310;  
 Best Local Similarity 77.8%; Pred. No. 27;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 DKATFGTHD 10  
 I : |||||  
 Db 362 DNASFGTHD 370

RESULT 5  
 T01265  
 starch synthase DULL1 - maize  
 C:Species: Zea mays (maize)  
 C:Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 29-Oct-1999  
 C:Accession: T01265  
 R:Gao, M.; Wanat, J.; Stinard, P.S.; James, M.G.; Myers, A.M.  
 Plant Cell 10, 399-412, 1998  
 A:Title: Characterization of dull1, a maize gene coding for a novel starch synthase.  
 A:Reference number: Z14287; MUID:98169346; PMID:9501113  
 A:Accession: T01265  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-1674 <GAO>  
 A:Cross-references: EMBL:AF023159; NID:g3057119; PIDN:AAC14014.1; PID:g3057120  
 C:Genetics:  
 A:Gene: dull1  
 A:Map position: 10

Query Match 57.5%; Score 42; DB 2; Length 1674;  
 Best Local Similarity 72.7%; Pred. No. 34;  
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 KDKATFGTHG 11  
 I : |||||  
 Db 611 KQLATVGTGHD 621

RESULT 6  
 NBRT  
 apolipoprotein H precursor - rat  
 N:Alternate names: beta-2-glycoprotein I  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 22-Jun-1999  
 C:Accession: S05310  
 R:Aoyama, Y.; Chan, Y.L.; Wool, I.G.  
 Nucleic Acids Res. 17, 6401, 1989  
 A:Title: The primary structure of rat beta(2)-glycoprotein I.  
 A:Reference number: S05310; MUID:89366680; PMID:2771694  
 A:Accession: S05310  
 A:Molecule type: mRNA  
 A:Residues: 1-297 <AOY>  
 A:Cross-references: EMBL:X1551; NID:g57524; PIDN:CAA33556.1; PID:g57525  
 A:Note: the authors translated the codon CAA for residue 148 as Glu and GAA for residue 149.  
 C:Comment: This plasma glycoprotein is a constituent of chylomicrons, VLDL, and HDL and has activity, and binds heparin. It may prevent activation of the intrinsic blood coagulation cascade.  
 C:Superfamily: apolipoprotein H; complement factor H repeat homology <FH3>  
 C:Keywords: chylomicron; duplication; glycoprotein; HDL; heparin binding; lipid binding;  
 F:1-19/Domain: signal sequence #status predicted <SIG>  
 F:20-297/Product: apolipoprotein H #status predicted <NAT>  
 F:36-89/Domain: complement factor H repeat homology <FH1>  
 F:94-152/Domain: complement factor H repeat homology <FH2>  
 F:157-212/Domain: complement factor H repeat homology <FH3>  
 F:216-277/Domain: complement factor H repeat homology <FH4>  
 F:36-76,62-89,94-140,126-152,157-200,186-212,216-267,252-259,277-297/Disulfide bonds: #  
 F:114,135,145,205/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 56.2%; Score 41; DB 1; Length 297;  
 Best Local Similarity 70.0%; Pred. No. 8.9;  
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KDKATFGTHD 10  
 I ||| I I I

Db 179 KDAVFGCHE 188

RESULT 7  
 JN0465  
 apolipoprotein H precursor - dog  
 N:Alternate names: beta 2 glycoprotein I  
 C:Species: Canis lupus familiaris (dog)  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C:Accession: JN0465; S32693  
 R:Sellar, G.C.; Keane, J.; Mehdi, H.; Peeples, M.E.; Browne, N.; Whitehead, A.S.  
 Biochem. Biophys. Res. Commun. 191, 1288-1293, 1993  
 A:Title: Characterization and acute phase modulation of canine apolipoprotein H (beta 2-glycoprotein I)  
 A:Reference number: JN0465; MUID:93221500; PMID:7692067  
 A:Accession: JN0465  
 A:Molecule type: mRNA  
 A:Residues: 1-345 <SEL>  
 A:Cross-references: EMBL:X72933; NID:g296088; PIDN:CAA51438.1; PID:g296089  
 A:Experimental source: liver  
 C:Comment: This plasma glycoprotein is a constituent of chylomicrons, VLDL, and HDL. It has blood coagulation cascade and ADP-mediated platelet aggregation.  
 C:Superfamily: apolipoprotein H; complement factor H repeat homology <FH3>  
 C:Keywords: chylomicron; duplication; glycoprotein; HDL; heparin binding; lipid binding;  
 F:1-19/Domain: signal sequence #status predicted <SIG>  
 F:20-345/Product: apolipoprotein H #status predicted <NAT>  
 F:23-79/Domain: complement factor H repeat homology <FH1>  
 F:84-137/Domain: complement factor H repeat homology <FH2>  
 F:142-200/Domain: complement factor H repeat homology <FH3>  
 F:205-260/Domain: complement factor H repeat homology <FH4>  
 F:264-325/Domain: complement factor H repeat homology <FH5>  
 F:301-306/Region: phospholipid binding #status predicted  
 F:23-66,51-79,84-124,110-137,142-188,174-200,203-248,234-260,264-315,300-307,325-345/  
 F:117,162,183,193,253/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 56.2%; Score 41; DB 1; Length 345;  
 Best Local Similarity 70.0%; Pred. No. 10;  
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KDKATFGTHD 10  
 I ||| I I I  
 Db 227 KDKAMYGCHD 236

RESULT 8  
 NBBO  
 apolipoprotein H precursor - bovine  
 N:Alternate names: beta-2-glycoprotein I; heparin-binding protein, 46K  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 30-Jun-1993 #sequence\_revision 19-May-1995 #text\_change 21-Jul-2000  
 C:Accession: JN0502; S23597; A43209; A39300; S09032  
 R:Gao, B.; Virmani, M.; Romm, E.; Lazar-Weasley, E.; Sakaguchi, K.; Appela, E.; Kunos, Gene 126, 287-288, 1993  
 A:Title: Sequence of a cDNA encoding bovine apolipoprotein H.  
 A:Reference number: JN0502; MUID:93246260; PMID:8482546  
 A:Accession: JN0502  
 A:Molecule type: mRNA  
 A:Residues: 1-100, 'G', 102-107, 'S', 109-176, 'R', 178-193, 'C', 195-258, 'N', 260-301, 'N', 303  
 A:Cross-references: GB:L07303; NID:g162679; PIDN:AAA30382.1; PID:g162680  
 A:Accession: PNO465  
 A:Molecule type: protein  
 A:Residues: 20-49 <GAI>  
 R:Bendixen, E.; Halkier, T.; Magnusson, S.; Sottrup-Jensen, L.; Kristensen, T.  
 Biochemistry 31, 3611-3617, 1992  
 A:Title: Complete primary structure of bovine beta(2)-glycoprotein I: localization of  
 A:Reference number: S23597; MUID:92232647; PMID:1567819  
 A:Accession: S23597  
 A:Molecule type: mRNA  
 A:Residues: 4-345 <BE2>  
 A:Cross-references: EMBL:X60065; NID:g5; PIDN:CAA42669.1; PID:g6  
 A:Accession: A43209  
 A:Molecule type: protein  
 A:Residues: 20-58;63-100;108-110;124-145;150-163;174-201;203-217;228-253, 'X', 255-256,  
 A:Note: 186-Glu was also found

R;Kato, H.; Enjyoji, K.  
 Biochemistry 30, 11687-11694, 1991  
 A:Title: Amino acid sequence and location of the disulfide bonds in bovine beta2 glycoprotein  
 A:Reference number: A39300; MUID:92089075; PMID:1751487  
 A:Accession: A39300  
 A:Molecule type: protein  
 A:Residues: 20-301, N, 303-345 <KAT>  
 R;Li, Q.; Blacher, R.; Esch, F.; Congote, L.F.  
 Biochem. J. 267, 261-264, 1990  
 A:Title: Isolation from fetal bovine serum of an apolipoprotein-H-like protein which inhibits lipoprotein lipase activity  
 A:Reference number: S09032; MUID:90226328; PMID:2327984  
 A:Accession: S09032  
 A:Molecule type: protein  
 A:Residues: 20-22, X', 24-41 <LIO>  
 C:Comment: This plasma glycoprotein is a constituent of chylomicrons, VLDL, and HDL and has lipase activity, and binds heparin. It may prevent activation of the intrinsic blood coagulation system  
 C:Superfamily: apolipoprotein H; complement factor H repeat homology  
 C:Keywords: chylomicron; duplication; glycoprotein; HDL; heparin binding; lipid binding; F1-19/DNAin: signal sequence (fragment) #status predicted <SIG>  
 F:20-345/Product: apolipoprotein H #status experimental <MAT>  
 F:23-79/DNAin: complement factor H repeat homology <FHL>  
 F:84-137/DNAin: complement factor H repeat homology <FHL>  
 F:142-200/DNAin: complement factor H repeat homology <PH3>  
 F:205-260/DNAin: complement factor H repeat homology <PH3>  
 F:264-325/DNAin: complement factor H repeat homology <PH5>  
 F:23-66, 51-79, 84-124, 110-137, 142-188, 174-200, 205-248, 234-260, 264-315, 300-325, 307-345/DNAin: complement factor H repeat homology <PH5>  
 F:92, 162, 183, 193, 253/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 54.8%; Score 40; DB 1; Length 345;  
 Best Local Similarity 70.0%; Pred. No. 16;  
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 KDKATFGTHD 10  
 DB 227 KDTATFGCHE 236  
 || ||||| I:  
 || ||||| I:

RESULT 9  
 S35733  
 DNA-directed DNA polymerase (EC 2.7.7.7) III beta chain - Spiroplasma citri  
 N:Alternate names: dnan  
 C:Species: Spiroplasma citri  
 C:Date: 13-Jan-1995 #sequence\_revision 16-Aug-1996 #text\_change 07-Dec-1999  
 C:Accession: S35733  
 R;Fie, F.; Laigret, F.; Bove, J.  
 submitted to the EMBL Data Library, December 1992  
 A:Description: Nucleotide sequence and genetic organization at the replication origin (ORI) of the plasmid pSPC1  
 A:Reference number: S35732  
 A:Accession: S35733  
 A:Molecule type: DNA  
 A:Residues: 1-363 <YEF>  
 A:Cross-references: EMBL:Z19108; NID:949345; PIDN:CAA79522.1; PID:949347  
 C:Genetics:  
 A:Gene: dnan  
 A:Genetic code: SGC3  
 C:Superfamily: DNA-directed DNA polymerase III beta chain  
 C:Keywords: DNA replication initiation; nucleotidyltransferase

Query Match 54.8%; Score 40; DB 1; Length 363;  
 Best Local Similarity 72.7%; Pred. No. 17;  
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 KDKATFGTHD 11  
 DB 39 KDKITFTSDG 49  
 ||||| I:  
 ||||| I:

RESULT 10  
 S86151  
 Hypothetical protein F22M8.9 - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Dec-2001  
 C:Accession: S86151

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.  
 Nature 408, 816-820, 2000  
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
 A:Reference number: A86141; MUID:21016719; PMID:11130712  
 A:Accession: E86151  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-1750 <STO>  
 A:Cross-references: GB:AE005172; NID:98570447; PIDN:AAF76474.1; GSPDB:GN00141  
 C:Genetics:  
 A:Map position: 1

Query Match 54.8%; Score 40; DB 2; Length 1750;  
 Best Local Similarity 77.8%; Pred. No. 83;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 3 KATFGTHD 11  
 DB 264 KGTFGGHDG 272  
 ||||| I:  
 ||||| I:

RESULT 11  
 H84298  
 2',3'-cyclic-nucleotide 2'-phosphodiesterase [imported] - Halobacterium sp. NRC-1  
 C:Species: Halobacterium sp. NRC-1  
 C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001  
 C:Accession: H84298  
 R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Laaky Jung, K.H.; Alam, M.; Freitas, T.  
 Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000  
 A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; A:Title: Genome sequence of Halobacterium species NRC-1.  
 A:Reference number: A84160; MUID:20504483; PMID:11016950  
 A:Accession: H84298  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-391 <STO>  
 A:Cross-references: GB:AE004437; NID:gi0580946; PIDN:AGL19756.1; GSPDB:GN00138  
 C:Genetics:  
 A:Gene: yfkN

Query Match 53.4%; Score 39; DB 2; Length 391;  
 Best Local Similarity 77.8%; Pred. No. 27;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 DKATFGTHD 10  
 DB 10 DVATFGNHD 18  
 ||||| I:  
 ||||| I:

RESULT 12  
 S28707  
 Hypothetical protein 25 - Agrobacterium tumefaciens plasmid pTi15955  
 C:Species: Agrobacterium tumefaciens  
 C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 08-Oct-1999  
 C:Accession: S28707  
 R;Barker, R.F.; Idler, K.B.; Thompson, D.V.; Kemp, J.D.  
 Plant Mol. Biol. 2, 335-350, 1983  
 A:Title: Nucleotide sequence of the T-DNA region from the Agrobacterium tumefaciens O A:Reference number: S28683  
 A:Accession: S28707  
 A:Status: translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-430 <BAR>  
 A:Cross-references: EMBL:X00493; NID:939062; PIDN:CAA25187.1; PID:939087

## C:Genetics:

A:Genome: plasmid  
C:Superfamily: short-chain alcohol dehydrogenase homology  
F:200-377/Domain: short-chain alcohol dehydrogenase homology <SADH>

Query Match 53.4%; Score 39; DB 2; Length 430;  
Best Local Similarity 85.7%; Pred. No. 30;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 FGTHDGG 12

|||||

Db 110 FGTHEGG 116

## RESULT 13

JC7582

armadillo(arm) repeat protein ALEX1 - human

C:Species: Homo sapiens (man)  
C:Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 30-Jun-2001

C:Accession: JC7582

R:Kurochkin, I.V.; Yonemitsu, N.; Funahashi, S.; Nomura, H.

Biochem. Biophys. Res. Commun. 280, 340-347, 2001

A:Title: ALEX1, a novel human armadillo repeat protein that is expressed differentially  
A:Reference number: JC7582; MUID: 21092608; PMID:11162520

C:Accession: JC7582

A:Molecule type: mRNA

A:Residues: 1-453 &lt;KUR&gt;

A:Cross-references: DBJ:AB039670

C:Comment: This protein is involved in regulation of normal cell growth, cell-to-cell si  
C:Genetics:

A:Gene: alex1

A:Map position: Xq21.33-q22.2

C:Keywords: tandem repeat; transmembrane protein

Query Match 53.4%; Score 39; DB 2; Length 453;  
Best Local Similarity 58.3%; Pred. No. 32;  
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 KDKATFGTHDGG 12

|||||

Db 91 KEKAHSGSHSGG 102

## RESULT 14

G84771

probable acyl-CoA oxidase [Imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 16-Feb-2001

C:Accession: G84771

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.  
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

C:Accession: G84771

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-664 &lt;STO&gt;

A:Cross-references: GB:AE002093; NID:94263786; PIDN:AAD15446.1; GSPDB:GN00139

C:Genetics:

A:Gene: At2g35690

A:Map position: 2

C:Superfamily: acyl-CoA oxidase

Query Match 53.4%; Score 39; DB 2; Length 664;  
Best Local Similarity 85.7%; Pred. No. 47;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 FGTHDGG 12

|||||

Db 313 FGSHDGG 319

## RESULT 15

AI0074

Probable autotransporter protein yapF [Imported] - Yersinia pestis (strain CO92)  
C:Species: Yersinia pestis

C:Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 02-Nov-2001

C:Accession: AI0074

R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.  
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.

ll, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel  
Nature 413, 523-527, 2001

A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A:Reference number: AB0001; MUID:21470413; PMID:11586360

A:Accession: AI0074

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-761 &lt;KUR&gt;

A:Cross-references: GB:AL590842; PIDN:CAC89460.1; PID:915978696; GSPDB:GN00175

C:Genetics:

A:Gene: yapF

Query Match 53.4%; Score 39; DB 2; Length 761;

Best Local Similarity 64.3%; Pred. No. 54;

Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 KDKATFGTHDGGXA 14

|||||

Db 714 KDKTQGTFFDLGMA 727

Search completed: August 28, 2003, 18:39:07

Job time : 14.1515 secs